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DETERMINANTS OF HOST SPECIES RANGE IN PLANT VIRUSES

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BACKGROUND and OBJECTIVES

Prediction of pathogen emergence is an important issue, both in human health and agronomy. Strikingly, most studies of pathogen emergence have focused on the responsible ecological or anthropogenic factors rather than on the role of intrinsic pathogen properties.

MATERIAL and METHODS

By focusing on a plant virus database (Brunt et al. 1996), we looked at the relationships between different virus characteristics (genome type, number of segments, type of vertical and horizontal transmissions, vector type, vection type) and the virus plant species range breadth.

RESULTS

We found that four main viral characteristics were strongly linked to virus host range breadth. Viruses (i) with single-stranded genomes (either RNA or DNA), (ii) with bipartite or tripartite genomes, (iii) that were seed transmitted and/or (iv) transmitted by nematodes presented a broader host range than others.

CONCLUSIONS

Viruses harboring these characteristics thus seem to be more prone to emerge in new host species. A statistical model was built that predicts host range breadth based on these four characteristics and could be used to focus quarantine processes and surveillances.

REFERENCES

Brunt, A.A., Crabtree, K., Dallwitz, M.J., Gibbs, A.J., and Watson, L. (eds). 1996. Viruses of plants: descriptions and lists from the VIDE database. 1484 pp. CAB International, Wallingford.

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